

Multifractal analysis of perceptron learning with errors

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Random input patterns induce a partition of the coupling space of a perceptron into cells labeled by their output sequences. Learning some data with a maximal error rate leads to clusters of neighboring cells. By analyzing the internal structure of these clusters with the formalism of multifractals, we can handle different storage and generalization tasks for lazy students and absent-minded teachers within one unified approach. The results also allow some conclusions on the spatial distribution of cells.

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I. INTRODUCTION

Artificial neural networks show considerable information processing capabilities, see e.g. [1]. One of the most important tasks is *classification* of data according to an initially unknown rule. Considering a set of $p = \gamma N$ input patterns $\xi^\mu \in \mathbb{R}^N, \mu = 1, \dots, p$, there are 2^p possible binary functions $\xi^\mu \mapsto \sigma^\mu = \pm 1$. Some of them are linearly separable and can be realized by a simple perceptron

$$\sigma = \text{sgn}(\mathbf{J} \cdot \boldsymbol{\xi}) = \text{sgn}\left(\sum_i J_i \xi_i\right) \quad (1)$$

where $\mathbf{J} \in \mathbb{R}^N$ is called the *coupling vector*. Due to the scaling invariance of (1) this vector can be restricted by the *spherical constraint* $\mathbf{J} \cdot \mathbf{J} = N$. The direction of \mathbf{J} fixes the actual form of the classification.

Not all coupling vectors define different functions of the p input patterns. According to their possible output sequences $\boldsymbol{\sigma} = \{\sigma^\mu | \mu = 1, \dots, p\}$ we can group them together into at most 2^p *cells*

$$C(\boldsymbol{\sigma}) = \{\mathbf{J} | \sigma^\mu = \text{sgn}(\mathbf{J} \cdot \boldsymbol{\xi}^\mu) \forall \mu\}. \quad (2)$$

These cells form a partition of the coupling space whose structure contains important information on the performance of the perceptron in various supervised learning problems.

The use of statistical mechanics in the study of the coupling space for large N was initiated by Gardner [2] for random input-output relations. Derrida et al. [3] suggested calculating the *cell size distribution*, which could be done only two years later when Monasson and O'Kane [4] introduced a modification of the standard replica trick in connection with multifractal techniques. Now there are several applications for perceptrons [5–8] and multilayer networks [9,10].

All these calculations consider the case where a uniquely determined output is perfectly learned by the student network. However, there is often no need or no possibility of perfect learning a special classification, or in real applications only noisy output data are available. Introducing an error rate corresponds to collecting several cells (2) into clusters. In the present paper we use the multifractal approach to characterize the coupling space structure of the output representations in these clusters. This analysis allows us to observe various storage and generalization problems within one approach. We include both the case of a student who perfectly learns some incorrect data (e.g. generalization with output noise) as well as the case of a student who tries to learn a well-defined task only with a certain error rate (e.g. storage with minimal error above the storage capacity).

The outline of the paper is as follows. In Sec. II we present the multifractal formalism for neural networks. Sec. III contains the general calculations for the internal representations of the cell clusters. In Sec. IV and V the most interesting cases are analyzed in detail, i.e. the storage and the generalization problems with noise. In Sec. VI we briefly comment on the spatial distribution of the cells. A summary is given in the final section.

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II. THE MULTIFRACTAL FORMALISM

Due to the geometrical nature of our problem a multifractal method is the appropriate one. In this section we introduce the multifractal formalism as applied to perceptrons. In order to clarify the notation we review some results obtained in [5,6] for spherical couplings without going into the subtleties of the approach.

We choose $p = \gamma N$ input patterns $\xi^\mu \in \{-1, 1\}^N$, $\mu = 1, \dots, p$, with entries randomly drawn from the distribution $p(\xi_i^\mu) = 1/2 \delta(\xi_i^\mu + 1) + 1/2 \delta(\xi_i^\mu - 1)$. The hyperplane perpendicular to each ξ^μ cuts the coupling space into two parts. The patterns therefore generate a random partition of the coupling space into cells defined by (2) and labeled by their output sequences σ . The relative cell size $P(\sigma) = V(\sigma) / \sum_\tau V(\tau)$ describes the probability of generating the output σ for a given input sequence ξ^μ with a coupling vector \mathbf{J} chosen at random from a uniform distribution over the whole coupling sphere. In the thermodynamic limit they are expected to scale exponentially with N , consequently we characterize the cell sizes by the *crowding index* $\alpha(\sigma)$ defined by

$$P(\sigma) = 2^{-N\alpha(\sigma)}. \quad (3)$$

The storage and generalization properties of the perceptron are coded in the *distribution of cell sizes* defined by

$$f(\alpha) = \lim_{N \rightarrow \infty} \frac{1}{N} \log_2 \sum_{\sigma} \delta(\alpha - \alpha(\sigma)). \quad (4)$$

In the language of multifractals this quantity is called the *multifractal spectrum*. To calculate it within the framework of statistical mechanics one uses the formal analogy of $f(\alpha)$ with the micro-canonical entropy of the spin system σ with Hamiltonian $N\alpha(\sigma)$. It can hence be determined from the corresponding ‘free energy’

$$\tau(p) = - \lim_{N \rightarrow \infty} \frac{1}{N} \log_2 \sum_{\sigma} 2^{-pN\alpha(\sigma)} = - \lim_{N \rightarrow \infty} \frac{1}{N} \log_2 \sum_{\sigma} P^p(\sigma) \quad (5)$$

via Legendre-transformation with respect to the ‘‘inverse temperature’’ p

$$f(\alpha) = \min_p [\alpha p - \tau(p)]. \quad (6)$$

In the multifractal terminology $\tau(p)$ is called the *mass exponent*.

To explicitly calculate this quantity for the perceptron we start with the definition of the cell size

$$P(\sigma) = \int d\mu(\mathbf{J}) \prod_{\mu=1}^p \theta\left(\frac{1}{\sqrt{N}} \sigma^\mu \mathbf{J} \cdot \xi^\mu\right) \quad (7)$$

using the Heaviside step function $\theta(x)$. The integral measure

$$d\mu(\mathbf{J}) = \prod_i \frac{dJ_i}{\sqrt{2\pi e}} \delta(N - \mathbf{J}^2). \quad (8)$$

ensures both the spherical constraint for the coupling vectors as well as the total normalization $\sum_{\sigma} P(\sigma) = 1$.

In the thermodynamic limit $N \rightarrow \infty$ we expect both τ and f to become self-averaging, and we can therefore calculate the mass exponent (5) by using the replica trick introducing n identical replicas numbered $a = 1, \dots, n$ to perform the average over the quenched patterns. Moreover, we introduce a second replica index $\alpha = 1, \dots, p$ in order to represent the p -th power of P in (5). Using an integral representation for the Heaviside function we arrive at a replicated partition function given by

$$\begin{aligned} Z_n &= \langle\langle Z^n \rangle\rangle \\ &= \langle\langle \sum_{\{\sigma_\mu^a\}} \int \prod_{a,\alpha} d\mu(\mathbf{J}_a^\alpha) \prod_{\mu,a,\alpha} \theta\left(\frac{\sigma_\mu^a}{\sqrt{N}} \mathbf{J}_a^\alpha \cdot \xi^\mu\right) \rangle\rangle \\ &= \langle\langle \sum_{\{\sigma_\mu^a\}} \int \prod_{a,\alpha} d\mu(\mathbf{J}_a^\alpha) \int_0^\infty \prod_{\mu,a,\alpha} \frac{d\lambda_{\mu,a}^{a,\alpha}}{\sqrt{2\pi}} \int \prod_{\mu,a,\alpha} \frac{dx_{\mu,a}^{a,\alpha}}{\sqrt{2\pi}} \\ &\quad \exp \left\{ i \sum_{\mu,a,\alpha} x_{\mu,a}^{a,\alpha} (\lambda_{\mu,a}^{a,\alpha} - \frac{\sigma_\mu^a}{\sqrt{N}} \mathbf{J}_a^\alpha \cdot \xi^\mu) \right\} \rangle\rangle. \end{aligned} \quad (9)$$

As usual, the average $\langle\langle \cdot \rangle\rangle$ over the quenched patterns can be performed, and the overlaps

$$P_{a,b}^{\alpha,\beta} = \frac{1}{N} \mathbf{J}_a^\alpha \cdot \mathbf{J}_b^\beta \quad (10)$$

are introduced as order parameters. The spherical constraint restricts the diagonal elements of this matrix to one.

It is important to note that the output sequences $\{\sigma_\mu^a\}$ carry only one replica index. The typical overlap of two coupling vectors within one cell (same output sequence $\{\sigma_\mu^a\}$) will hence in general be different from the typical overlap between two coupling vectors belonging to different cells (different output sequence $\{\sigma_\mu^a\}$). Therefore we have to introduce already within the *replica symmetric approximation* two different overlap values:

$$P_{a,b}^{\alpha,\beta} = \begin{cases} 1 & \text{if } (a, \alpha) = (b, \beta) \\ P & \text{if } a = b, \alpha \neq \beta \\ P_0 & \text{if } a \neq b \end{cases} . \quad (11)$$

In accordance with the above discussion P then denotes the typical overlap *within one cell*, whereas P_0 denotes the overlap *between different cells*.

Plugging this RS ansatz into (9) one realizes that $P_0 = 0$ always solves the saddle point equations for P_0 . This has an obvious physical interpretation: Due to the symmetry of (1) and therefore of the crowding index under the transformation $(\mathbf{J}, \boldsymbol{\sigma}) \leftrightarrow (-\mathbf{J}, -\boldsymbol{\sigma})$ every cell has a “mirror cell” of same size and shape on the “opposite side” of the coupling space. $P_0 = 0$ simply reflects this symmetry.

Finally we obtain the mass exponent

$$\tau(p) = -\frac{1}{\log 2} \text{extr}_P \left[\frac{1}{2} \log(1 + (p-1)P) - \frac{p-1}{2} \log(1-P) - \gamma \log 2 \int DtH^p \left(\sqrt{\frac{P}{1-P}} t \right) \right] \quad (12)$$

where we introduced the abbreviations $Dt = dt \exp(-t^2/2)/\sqrt{2\pi}$ for the Gaussian measure and $H(x) = \int_x^\infty Dt$. The order parameter P is self-consistently determined by the saddle point equation

$$\frac{P}{1 + (p-1)P} = \frac{\gamma}{2\pi} \frac{\int DtH^{p-2} \left(\sqrt{\frac{P}{1-P}} t \right) \exp \left\{ -\frac{P}{1-P} t^2 \right\}}{\int DtH^p \left(\sqrt{\frac{P}{1-P}} t \right)} . \quad (13)$$

This equation can only be solved numerically, the results are shown in fig. 1.

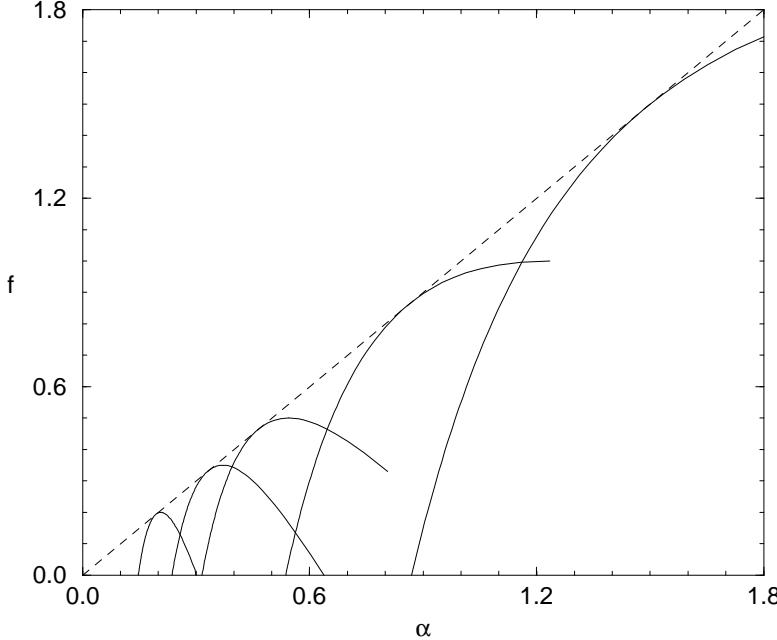


FIG. 1. Multifractal spectrum $f(\alpha)$ characterizing the cell structure of the coupling space of the spherical perceptron for various values of the loading parameter $\gamma = 0.2, 0.35, 0.5, 1.0, 2.0$ (from left to right).

The total number of cells is given by

$$\mathcal{N} = \int_0^\infty d\alpha 2^{Nf(\alpha)} \quad (14)$$

and is therefore exponentially dominated by cells of size $\alpha_0(\gamma) = \text{argmax}(f(\alpha))$. Because of $\frac{df}{d\alpha} = p$ this point is reached at $p = 0$. The random choice of any output sequence will hence lead with probability one to a cell of size $\alpha_0(\gamma)$, and $2^{-N\alpha_0(\gamma)}$ is found to be the Gardner volume. From $\alpha_0(\gamma \rightarrow 2) \rightarrow \infty$ we find the storage capacity to be $\gamma_c = 2$ as in [2]. For $\gamma < 2$ the problem of storing γN random input–output pairs is realizable with probability one. So we have $\mathcal{N} = 2^{\gamma N - o(N)}$ and therefore $f(\alpha_0(\gamma)) = \gamma$ in the thermodynamic limit.

Although the cells with volume α_0 are the most frequent ones, their joint contribution to the total *volume* of the sphere is negligible. Since

$$1 = \sum_{\sigma} P(\sigma) = \int_0^\infty d\alpha 2^{N[f(\alpha) - \alpha]} \quad (15)$$

a saddle point argument reveals that the cells with size $\alpha_1(\gamma)$ defined by $\frac{df}{d\alpha}(\alpha_1) = 1$ dominate the volume. This point is given by $p = 1$. Cells of larger size are too rare, those more frequent are too small to compete. Consequently a randomly chosen *coupling vector* \mathbf{J} will with probability one belong to a cell of size α_1 . By the definition (2) of the cells all other couplings of this cell will give the same output for all patterns ξ^μ . Therefore $2^{-N\alpha_1(\gamma)}$ is nothing but the volume of the version space of a teacher perceptron chosen at random from a uniform probability distribution on the sphere of possible perceptrons. From it (or equivalently from $P(p = 1, \gamma)$) one can determine the generalization error as a function of the training set size γ , thus reproducing the results of [11].

III. INTERNAL CELL STRUCTURE OF CLUSTERS FOR NOISY OUTPUT DATA

In order to include noisy output data we have to slightly modify this procedure. As before, we consider a randomly drawn set of input patterns $\{\xi^\mu; \mu = 1, \dots, \gamma N\}$ as quenched disorder. The global cell distribution consequently equals the one in the previous section.

Now we take any output sequence $\mathbf{s} \in \{-1, 1\}^{\gamma N}$, demanding it to be learned with an error rate $\delta \in (0, 0.5)$. $\delta = 0$ corresponds to the noise-free case, $\delta = 0.5$ to outputs which are totally uncorrelated to the original pattern \mathbf{s} . The realized output $\sigma \in \{-1, 1\}^{\gamma N}$ has an overlap

$$\frac{1}{\gamma N} \sum_{\mu=1}^{\gamma N} \sigma^\mu s^\mu = 1 - 2\delta \quad (16)$$

with \mathbf{s} . The set of all cells $C(\sigma)$ with this output overlap forms a cluster. It is the internal structure of the cluster which we will analyze, i.e. we calculate the internal cell spectrum of the cluster. The restricted partition function can be written as

$$Z(\mathbf{s}, \delta) = \sum_{\sigma} \delta \left(\frac{1}{\gamma N} \sum_{\mu=1}^{\gamma N} \sigma^\mu s^\mu - 1 + 2\delta \right) P^q(\sigma), \quad (17)$$

where the relative volume $P(\sigma)$ is defined by (7). In the special case of a randomly drawn sequence \mathbf{s} this quantity is closely related to the partition function considered in [12] where a Gibbs measure of the error rate was introduced instead of the δ -function in (17). Being self-averaging $Z(\mathbf{s}, \delta)$ does not depend on \mathbf{s} itself, but only on the size $\alpha(\mathbf{s})$ of the central cell. It can therefore be characterized by the real number p with $\alpha(\mathbf{s}) = \alpha_p$, $\frac{df}{d\alpha}(\alpha_p) = p$, in the global spectrum. The mass exponent of the cluster is thus given by

$$\tau(q|p, \delta) = - \lim_{N \rightarrow \infty} \frac{1}{N} \left(\left\langle \frac{\sum_{\mathbf{s}} P^p(\mathbf{s}) \log_2 Z(\mathbf{s}, \delta)}{\sum_{\mathbf{s}} P^p(\mathbf{s})} \right\rangle \right). \quad (18)$$

This is in complete analogy to the standard calculation of canonical expectation values in statistical mechanics. A very similar method was introduced in [13] in order to characterize metastable states in spherical p -spin glasses. In

that case one system was thermalized in an equilibrium state, whereas a second one was restricted to have a certain overlap with the first one – which is analogous to our output sequences \mathbf{s} and $\boldsymbol{\sigma}$.

The internal spectrum $f(\alpha|p, \delta)$ of the cluster can again be calculated by a Legendre transformation with respect to the ‘inverse temperature’ q , cf. (6).

Before explicitly performing the technical part of the analysis we want to clarify the question which problems can be solved within our approach. Clearly, the value of p fixes the original learning task without noise, which corresponds to perfect learning of the output sequence \mathbf{s} . As already discussed in Sec. II, $p = 0, 1$ are of particular importance for storage and generalization problems. Now, $q = 0$ describes the most frequent cell within the cluster. If we take any random output string $\boldsymbol{\sigma}$ having overlap $1 - 2\delta$ with \mathbf{s} , we will arrive with probability one in a cell of size $\alpha(q = 0|p, \delta)$. This point corresponds therefore to a student who perfectly learns one particular incorrect output sequence. For the generalization problem, $p = 1$, it gives the behavior in the presence of output noise.

On the other hand, $q = 1$ characterizes the volume-dominating cells of the cluster, the total crowding index of the cluster is given by

$$\alpha_{cl}(p, \delta) = \alpha(q = 1|p, \delta) - f(\alpha(q = 1|p, \delta)|p, \delta) \quad (19)$$

It describes the volume of the version space of a lazy student who is satisfied whenever he finds a coupling vector producing errors with maximal rate δ .

From the spectra for different p but fixed δ we can get some information on the spatial distribution of the cells – whether there are more large/small cells in the environment of another large/small cell. This can be read off the p -dependence of the internal cluster spectrum for one value of δ .

In order to answer all these questions we have to calculate the mass exponent (18). We need to introduce four replications as representation of:

- (i) the logarithm of the partition function: $a = 1, \dots, n$,
- (ii) the power q in the partition function: $\alpha = 1, \dots, q$,
- (iii) the fraction in the average over all p -cells: $k = 1, \dots, m$,
- (iv) the power p in the average over all p -cells: $\kappa = 1, \dots, p$.

The replicated and averaged partition function consequently reads

$$Z_{m,n} = \langle \langle \sum_{\mathbf{s}_k, \boldsymbol{\sigma}_a} \int \prod_{k,\kappa} d\mu(\mathbf{K}_k^\kappa) \prod_{\mu,k,\kappa} \Theta\left(\frac{s_k^\mu}{\sqrt{N}} \mathbf{K}_k^\kappa \cdot \boldsymbol{\xi}^\mu\right) \int \prod_{a,\alpha} d\mu(\mathbf{J}_a^\alpha) \prod_{\mu,a,\alpha} \Theta\left(\frac{\sigma_a^\mu}{\sqrt{N}} \mathbf{J}_a^\alpha \cdot \boldsymbol{\xi}^\mu\right) \prod_a \delta\left(\frac{1}{\gamma N} \mathbf{s}_1 \cdot \boldsymbol{\sigma}_a - 1 + 2\delta\right) \rangle \rangle . \quad (20)$$

The coupling vectors \mathbf{K}_k^κ are elements of the p -cells, \mathbf{K}_1^κ of the central cell of the cluster. \mathbf{J}_a^α lies within the cluster cells. Using this, the mass exponent can be determined from the replica trick

$$\tau(q|p, \delta) = - \lim_{N \rightarrow \infty} \frac{1}{N \ln 2} \lim_{m,n \rightarrow 0} \partial_n Z_{m,n} . \quad (21)$$

The calculation of $Z_{m,n}$ widely follows standard routes and uses the order parameters

$$\begin{aligned} P_{k,l}^{\kappa,\lambda} &= \frac{1}{N} \mathbf{K}_k^\kappa \cdot \mathbf{K}_l^\lambda, \quad \forall k, l = 1, \dots, m; \kappa, \lambda = 1, \dots, p \\ Q_{a,b}^{\alpha,\beta} &= \frac{1}{N} \mathbf{J}_a^\alpha \cdot \mathbf{J}_b^\beta, \quad \forall a, b = 1, \dots, n; \alpha, \beta = 1, \dots, q \\ R_{k,a}^{\kappa,\alpha} &= \frac{1}{N} \mathbf{K}_k^\kappa \cdot \mathbf{J}_a^\alpha \end{aligned} \quad (22)$$

for the overlaps of coupling vectors from p -cells and from q -cells of the cluster. The diagonal elements of the matrices \mathbf{Q} and \mathbf{P} are restricted to one by the spherical constraint. This leads after standard manipulations to

$$\begin{aligned} Z_{m,n} &= \int \prod_{(k,\kappa) < (l,\lambda)} dP_{k,l}^{\kappa,\lambda} \int \prod_{(a,\alpha) < (b,\beta)} dQ_{a,b}^{\alpha,\beta} \int \prod_{(k,\kappa), (a,\alpha)} dR_{k,a}^{\kappa,\alpha} \int \prod_a dF_a \\ &\times \exp \left\{ \frac{N}{2} \ln \det \begin{pmatrix} \mathbf{P} & \mathbf{R} \\ \mathbf{R}^t & \mathbf{Q} \end{pmatrix} + i\gamma N(1 - 2\delta) \sum_a F_a \right\} \\ &\times \left[\int_0^\infty \prod_{(k,\kappa)} d\rho_k^\kappa \int \prod_{(k,\kappa)} \frac{dy_k^\kappa}{2\pi} \int_0^\infty \prod_{(a,\alpha)} d\lambda_a^\alpha \int \prod_{(a,\alpha)} \frac{dx_a^\alpha}{2\pi} \sum_{s_k, \sigma_a} \right. \end{aligned}$$

$$\begin{aligned} & \times \exp \left\{ -\frac{1}{2} \sum_{a,\alpha,b,\beta} Q_{a,b}^{\alpha,\beta} x_a^\alpha x_b^\beta - \sum_{k,\kappa,a,\alpha} R_{k,a}^{\kappa,\alpha} y_k^\kappa x_a^\alpha - \frac{1}{2} \sum_{k,\kappa,l,\lambda} P_{k,l}^{\kappa,\lambda} y_k^\kappa y_l^\lambda \right. \\ & \left. + i \sum_{a,\alpha} \sigma_a \lambda_a^\alpha x_a^\alpha + i \sum_{k,\kappa} s_k \rho_k^\kappa y_k^\kappa + i \sum_a F_a \sigma_a s_1 \right\} \right]^{\gamma N}, \end{aligned} \quad (23)$$

where F_a was introduced to fix the overlap of s_1 and σ_a to $1 - 2\delta$.

The determinant can be represented by a Gaussian integral having the same exponent like the quadratic part of the second exponent in (23). By transforming the integration variable according to

$$y_k^\kappa \mapsto y_k^\kappa + \sum_{l,\lambda,a,\alpha} (\mathbf{P}^{-1})_{k,l}^{\kappa,\lambda} R_{l,a}^{\lambda,\alpha} x_a^\alpha \quad (24)$$

we obtain

$$\ln \det \begin{pmatrix} \mathbf{P} & \mathbf{R} \\ \mathbf{R}^t & \mathbf{Q} \end{pmatrix} = \ln \det \mathbf{P} + \ln \det (\mathbf{Q} - \mathbf{A}) \quad (25)$$

with $A_{a,b}^{\alpha,\beta} = \sum_{k,\kappa,l,\lambda} R_{k,a}^{\kappa,\alpha} (\mathbf{P}^{-1})_{k,l}^{\kappa,\lambda} R_{l,b}^{\lambda,\beta}$. The same transformation can be made in the second exponent in (23). We analyse the resulting expression using the replica symmetric ansatz:

$$\begin{aligned} P_{k,l}^{\kappa,\lambda} &= \begin{cases} 1 & (k,\kappa) = (l,\lambda) \\ P & k = l, \kappa \neq \lambda \\ 0 & k \neq l \end{cases} \\ Q_{a,b}^{\alpha,\beta} &= \begin{cases} 1 & (a,\alpha) = (b,\beta) \\ Q_1 & a = b, \alpha \neq \beta \\ Q_0 & a \neq b \end{cases} \\ R_{k,a}^{\kappa,\alpha} &= \begin{cases} R & k = 1 \\ 0 & k \neq 1 \end{cases} \end{aligned} \quad (26)$$

$$iF_a = F.$$

P describes the typical overlap within one p -cell of the global spectrum therefore fulfilling the saddle-point equation (13) from sec. II. Q_1 gives the overlap of two arbitrary couplings from the same q -cell inside the cluster, Q_0 the overlap between two of these cells. Due to the fixed overlap of the cluster output with the output of the central cell, the mirror symmetry $(\mathbf{J}, \boldsymbol{\sigma}) \mapsto (-\mathbf{J}, -\boldsymbol{\sigma})$ is explicitly broken, we therefore expect Q_0 to be different from zero. R is the overlap of the cluster cells with the central p -cell, whereas the overlap of a cell from the cluster with a randomly chosen p -cell is again zero for symmetry reasons.

Finally we get the replica symmetric mass exponent by taking the $O(n)$ -terms for $m = 0$,

$$\begin{aligned} \tau(q|p, \delta) = & -\frac{1}{\ln 2} \text{extr}_{Q_{0,1}, R, F} \left[\frac{q-1}{2} \ln(1 - Q_1) + \frac{1}{2} \ln(1 + (q-1)Q_1 - qQ_0) + \frac{q}{2} \frac{Q_0 - \frac{pR^2}{1-(p-1)P}}{1 + (q-1)Q_1 - qQ_0} + \gamma(1 - 2\delta)F \right. \\ & \left. + \gamma \frac{\int \frac{dc}{2\pi} \frac{d\hat{c}}{2\pi} e^{ic\hat{c}} \int Dt \left[\int_0^\infty \frac{d\rho}{\sqrt{2\pi(1-P)}} \exp\left\{-\frac{1}{2} \frac{(\rho - \sqrt{P}t)^2}{1-P} - i\hat{c}\rho\right\} \right]^p \int Du \ln \int Dw (e^F H_-^q + e^{-F} H_+^q)}{\int Dt H^p(\sqrt{\frac{P}{1-P}}t)} \right] \end{aligned} \quad (27)$$

with

$$H_\pm = H \left(\pm \frac{\sqrt{Q_1 - Q_0}w + \sqrt{Q_0 - \frac{pR^2}{1-(p-1)P}}u + \frac{R}{1+(p-1)P}c}{\sqrt{1 - Q_1}} \right). \quad (28)$$

P is given by (13) for p . Because of the integrals over complex-valued functions the general case is hard to handle numerically, and we concentrate on the most important cases $p = 0, 1$, i.e. the storage and generalization problems.

IV. STORAGE WITH ERRORS

This section we focus on the storage problem with noisy output data, i.e. the case of a central cell with $p = 0$. Inserting this into (27) we can eliminate the integrals over complex-valued functions and find

$$\begin{aligned} \tau(q|0, \delta) = -\frac{1}{\ln 2} \text{extr}_{Q_0, 1, F} \left[\frac{q-1}{2} \ln(1-Q_1) + \frac{1}{2} \ln(1+(q-1)Q_1 - qQ_0) + \frac{q}{2} \frac{Q_0}{1+(q-1)Q_1 - qQ_0} + \gamma(1-2\delta)F \right. \\ \left. + \gamma \int Du \ln \int Dw (e^F H_-^q + e^{-F} H_+^q) \right] \end{aligned} \quad (29)$$

where H_{\pm} simplifies to

$$H_{\pm} = H \left(\pm \frac{\sqrt{Q_1 - Q_0} w + \sqrt{Q_0} u}{\sqrt{1 - Q_1}} \right). \quad (30)$$

The dependences on R and P vanish, leading to only three saddle point equations for the order parameters Q_0, Q_1 , and F :

$$\begin{aligned} 0 &= 1 - 2\delta - \int Du \frac{\int Dw (e^F H_-^q - e^{-F} H_+^q)}{\int Dw (e^F H_-^q + e^{-F} H_+^q)} \\ 0 &= \frac{Q_0}{(1+(q-1)Q_1 - qQ_0)^2} - \frac{\gamma}{2\pi(1-Q_1)} \int Du \left[\frac{\int Dw (e^F H_-^{q-1} - e^{-F} H_+^{q-1}) \exp\left\{-\frac{(\sqrt{Q_1 - Q_0} w + \sqrt{Q_0} u)^2}{2(1-Q_1)}\right\}}{\int Dw (e^F H_-^q + e^{-F} H_+^q)} \right]^2 \\ 0 &= \frac{Q_1 - Q_0}{1+(q-1)Q_1 - qQ_0} + \frac{Q_0(1-Q_1)}{(1+(q-1)Q_1 - qQ_0)^2} - \frac{\gamma}{2\pi} \int Du \frac{\int Dw (e^F H_-^{q-2} + e^{-F} H_+^{q-2}) \exp\left\{-\frac{(\sqrt{Q_1 - Q_0} w + \sqrt{Q_0} u)^2}{1-Q_1}\right\}}{\int Dw (e^F H_-^q + e^{-F} H_+^q)} \end{aligned} \quad (31)$$

Before solving these equations numerically, we discuss some intuitively clear and also analytically tractable limiting cases. For $\delta = 0.5$ half the output bits are flipped and there is no remaining correlation between the original output sequence \mathbf{s} and the sequence $\boldsymbol{\sigma}$ to be learned. Up to terms irrelevant in the limit of large N we obtain at most $\binom{\gamma N}{0.5\gamma N} \simeq 2^{\gamma N}$ possible cells, the spectrum equals hence the global one described in Sec. II. From the first saddle point equation we calculate $F = 0$, from the second follows $Q_0 = 0$. The third equation together with (29) confirm our expectation.

For $\delta = 0$ both sequences \mathbf{s} and $\boldsymbol{\sigma}$ coincide up to a non-extensive fraction of bits. The cluster thus shrinks towards its central cell, which has the Gardner volume. The cluster spectrum shrinks to a single point at α_0 (as defined in Sec. II) and $f = 0$. In the saddle point equations (31) we find this result for $F \rightarrow -\infty$ and $Q_0 = Q_1 = P(p=0)$ fulfilling (13) with $p = 0$.

For $q = 0$ we obtain for every fixed δ the storage problem with an output sequence produced by flipping $\delta\gamma N$ bits randomly chosen from a randomly drawn sequence of length γN . The resulting output sequence $\boldsymbol{\sigma}$ is consequently also a random sequence of independent and unbiased bits. The learning problem is obviously equivalent to the standard Gardner problem. This is confirmed by $\alpha(q=0|0, \delta) = \alpha_0, \forall \delta$, whereas the total number of these cells is $\binom{\gamma N}{\delta\gamma N}$ resulting in $f(0|0, \delta) = -\gamma(\delta \log_2 \delta - (1-\delta) \log_2(1-\delta))$ in the thermodynamic limit.

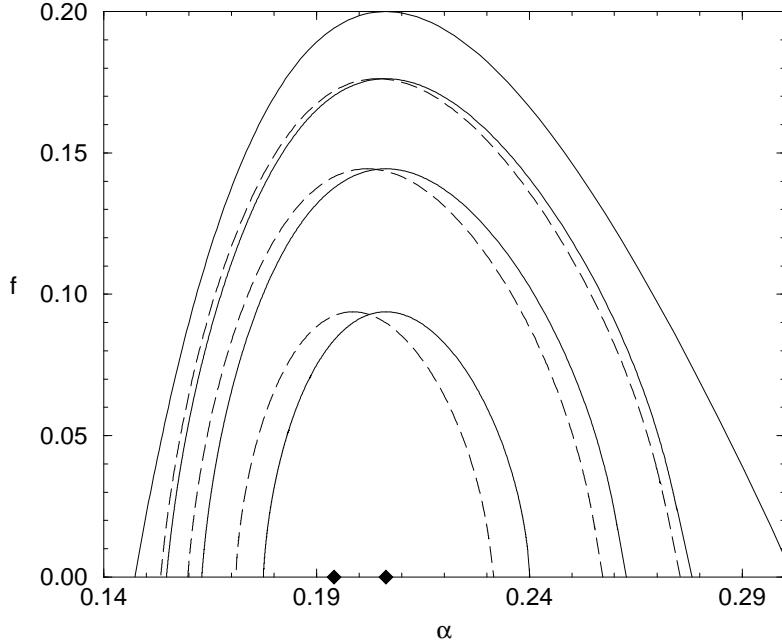


FIG. 2. Multifractal spectrum $f(\alpha)$ of clusters around p -cells with $p = 0, 1$ (solid/dashed lines) for $\gamma = 0.2$ and $\delta = 0.5, 0.3, 0.2, 0.1$ (from top). The diamonds mark the crowding indices of the central cells, they coincide with the spectra for $\delta = 0$.

The rest of the spectrum has to be analyzed numerically, a typical set of $f(\alpha)$ -curves is shown in fig. 2. The most interesting point is – besides $q = 0$ as discussed above – given by $q = 1$. The total volume of the cluster is given by its crowding index $\alpha_{cl}(\delta) = \alpha(q = 1|0, \delta) - f(\alpha(q = 1|0, \delta))$. By calculating the storage capacity $\gamma_c(\delta)$ for fixed error rate δ from the divergence of α_{cl} we reproduce the replica symmetric results of [2] which Gardner and Derrida calculated for the minimal error rate above $\gamma = 2$. So at least at that point, replica symmetry breaking effects should be taken into account in the ansatz for the cluster overlap \mathbf{Q} . However, due to the complexity of even the replica symmetric calculation we refrain from doing this.

We still have to remark that the continuation of the mass exponent to negative q is somewhat subtle. This can be expected already by considering the definition (17) of the restricted partition function $Z(\mathbf{s}, \delta)$. Whenever there are empty cells, (17) diverges for every $q < 0$, leading to $\tau(q < 0|p, \delta) = -\infty$ because of the average over all input realizations in (18). Without any change of the results for positive q we can regularize τ by summing only over those $\boldsymbol{\sigma}$ having a non vanishing relative cell volume $P(\boldsymbol{\sigma})$ – describing the well-defined multifractal spectrum also for $q < 0$ via a Legendre transformation.

We consider now the last integral in (29) in the case of negative q . Because of $H(w) \propto \exp(-w^2/2)/\sqrt{2\pi}w$ for large w we get an asymptotic exponential part of the last integrand which is proportional to $\exp(-\Delta w^2/2 + O(w))$ with

$$\Delta = \frac{1 + (q - 1)Q_1 - qQ_0}{1 - Q_1}. \quad (32)$$

The integral consequently diverges for $\Delta \geq 0$, i.e. for every $0 \leq Q_0 \leq 1$ at $Q_1 = (1 - qQ_0)/(1 - q)$, and the global minimum in (29) with respect to Q_1 is no longer given by the saddle point equations (31). Due to this the mass exponent would be expected to diverge to $-\infty$ for every $q < 0$. On the other hand, the continuation of the saddle point equations (31) to $q < 0$ gives smooth results for the mass exponent and the multifractal spectrum. We expect it therefore to describe the correct regularization of the partition function at least within the replica symmetric approximation.

V. GENERALIZATION WITH ERRORS

In this section we treat the question of generalizing noisy output data. As mentioned in Sec. II, this problem corresponds to taking $p = 1$. Also in this case the complex-valued integrals can be evaluated analytically. The mass exponent is given by

$$\begin{aligned} \tau(q|1, \delta) = -\frac{1}{\ln 2} \text{extr}_{Q_{0,1}, R, F} \left[\frac{q-1}{2} \ln(1-Q_1) + \frac{1}{2} \ln(1+(q-1)Q_1 - qQ_0) + \frac{q}{2} \frac{Q_0 - R^2}{1 + (q-1)Q_1 - qQ_0} + \gamma(1-2\delta)F \right. \\ \left. + 2\gamma \int Du H \left(\frac{uR}{\sqrt{Q_0 - R^2}} \right) \ln \int Dw (e^F H_-^q + e^{-F} H_+^q) \right] \end{aligned} \quad (33)$$

with

$$H_{\pm} = H \left(\pm \frac{\sqrt{Q_1 - Q_0} w + \sqrt{Q_0} u}{\sqrt{1 - Q_1}} \right). \quad (34)$$

Again, the dependence on P vanishes whereas R remains an order parameter to be optimized. We obtain four saddle point equations which determine Q_0 , Q_1 , R , and F :

$$\begin{aligned} 0 = 1 - 2\delta - 2 \int Du H \left(\frac{uR}{\sqrt{Q_0 - R^2}} \right) \frac{\int Dw (e^F H_-^q - e^{-F} H_+^q)}{\int Dw (e^F H_-^q + e^{-F} H_+^q)} \\ 0 = \frac{Q_0 - R^2}{(1 + (q-1)Q_1 - qQ_0)^2} - \frac{\gamma}{\pi(1 - Q_1)} \int Du H \left(\frac{uR}{\sqrt{Q_0 - R^2}} \right) \\ \times \left[\frac{\int Dw (e^F H_-^{q-1} - e^{-F} H_+^{q-1}) \exp\left\{-\frac{(\sqrt{Q_1 - Q_0} w + \sqrt{Q_0} u)^2}{2(1 - Q_1)}\right\}}{\int Dw (e^F H_-^q + e^{-F} H_+^q)} \right]^2 \\ 0 = \frac{Q_1 - Q_0}{1 + (q-1)Q_1 - qQ_0} + \frac{(Q_0 - R^2)(1 - Q_1)}{(1 + (q-1)Q_1 - qQ_0)^2} \\ - \frac{\gamma}{\pi} \int Du H \left(\frac{uR}{\sqrt{Q_0 - R^2}} \right) \frac{\int Dw (e^F H_-^{q-2} + e^{-F} H_+^{q-2}) \exp\left\{-\frac{(\sqrt{Q_1 - Q_0} w + \sqrt{Q_0} u)^2}{1 - Q_1}\right\}}{\int Dw (e^F H_-^q + e^{-F} H_+^q)} \\ 0 = \frac{qR}{1 + (q-1)Q_1 - qQ_0} + \frac{\gamma}{\pi} \int du e^{-\frac{Q_0 u^2}{2(Q_0 - R^2)}} \frac{Q_0 u}{(Q_0 - R^2)^{3/2}} \ln \int Dw (e^F H_-^q + e^{-F} H_+^q). \end{aligned} \quad (35)$$

Several intuitively clear limiting cases can be discussed analytically. As argued in the previous section, for $\delta = 0.5$ we recover the full spectrum with order parameters $F = 0$, $R = 0$, $Q_0 = 0$ and $Q_1 = P(q)$. R is the overlap of the central cell with the cells of the cluster. Its value is found to be zero for all q indicating that all types of cluster cells are orthogonal to the teacher vector, their volumes are dominated by the part lying on the $(N-1)$ -dimensional “equator”. The learning of a vector obtained by flipping half of the teacher’s outputs is obviously equivalent to the storage problem of a random output sequence. The student is not able to get any information about the teachers rule.

For $\delta \rightarrow 0$ the cell cluster shrinks towards the central cell, which is the version space of the corresponding noise-free generalization problem. F diverges to $-\infty$ whereas the other three order parameters coincide asymptotically, $Q_0 = Q_1 = R = P(p=1)$. The crowding index takes only the value α_1 , $f(q|1, 0)$ is found to be zero. The equivalence of this solution to earlier results of [11] was already discussed in [5,6].

For general δ the analysis has to be done numerically. In fig. 1 we show a representative set of spectra for several values of δ . For growing error rate not only the number of cells in the cluster increases, but also the range of different existent cell sizes.

For $q = 0$ we obtain a student who perfectly learns an output sequence generated by a teacher, but flipped with rate δ . This corresponds to the case of output noise analyzed in [11,14]. The cell sizes go for $0 < \delta < 0.5$ from α_1

to α_0 , thus interpolating between the noiseless learning from examples and the storage problem for random input–output relations. This interpretation gives also a sense to the part of the global cell spectrum for inverse temperatures between zero and one, at least a proper subset of these can be understood as generalization tasks including noisy output data. Of course, for $\delta > 0$ this task is not learnable for large loading ratios γ . This observation leads directly to a storage capacity $\gamma_c(\delta)$ going monotonously from $\gamma_c(0) = \infty$ to the Gardner value $\gamma_c(\delta = 0) = 2$. For every δ the overlap R between teacher and student is a monotonously increasing function of the loading ratio. Its maximal value is reached at $R_{max}(\delta) = R(\gamma_c(\delta))$ which remains strictly smaller then one for every $\delta \neq 0$.

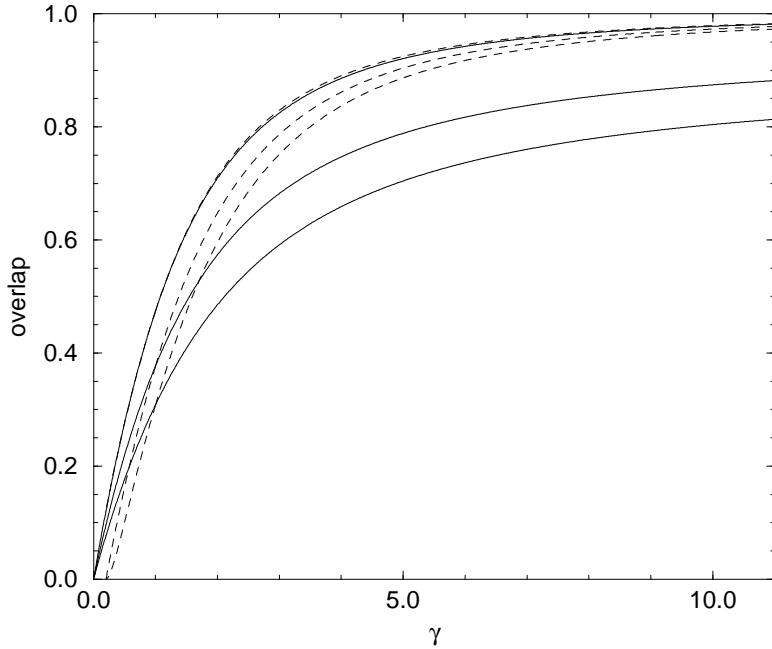


FIG. 3. Overlaps Q_1, R, Q_0 (from top to bottom) for the generalization problem with a student making up to $0.1\gamma N$ (full lines) and $0.1N$ (dashed lines) errors

Another problem can be analyzed in the spectrum at $q = 1$. The total volume of the cell cluster surrounding a cell of size α_1 is given by its total crowding index which can again be calculated from $\alpha_{cl}(\delta) = \alpha(q = 1|1, \delta) - f(\alpha(q = 1|1, \delta))$. This learning task corresponds to a lazy student being satisfied with any output having at most $\delta\gamma N$ errors compared with the sequence of examples presented by the teacher, cf. [11]. The student can achieve this for every value of γ , an upper threshold for the loading ratio does not exist. As illustrated by the full lines in fig. 3, in the case of a fixed error rate $\delta > 0$ the overlap R between teacher and student does not go to one, and the generalization error $\varepsilon = \frac{1}{\pi} \arccos R$ does not tend to zero for increasing loading ratio γ . The cell volume of every special output realization shrinks to zero, $Q_1 \rightarrow 1$, but this is compensated by a cell number exponentially growing with γN . Thus, the resulting total cluster volume does not vanish, $Q_0 < 1$. If we fix instead the total number of errors, the number of possible representations does not depend on γ either. The vanishing version space volume of every particular output sequence thus results in a vanishing total volume, leading to a vanishing generalization error in the limit of large loadings γ , cf. the dashed lines in figure 3. In both cases, the information gain [14] $\partial\alpha_{cl}/\partial\gamma$ goes from values of order one (halving the cell with every new pattern) for small γ to zero for $\gamma \rightarrow \infty$.

The inclusion simultaneous noise for teacher and student requires the introduction of 6 different replications resulting in an even more complex structure of the order parameter equations. Therefore we refrain from doing it.

VI. ON THE SPATIAL CELL DISTRIBUTION

From the spectrum of the internal representations in a cluster we can also get some information on the spatial distribution of the cells. If the latter were totally random, we would not expect any dependence of the internal cluster spectrum on the central cell, i.e. on p . In this case, cells of all possible sizes should be contained in the cluster. From

fig. 1, where the spectra are plotted for $p = 0, 1$, we can deduce that the distribution has some structure. Reducing δ from 0.5 does not only decrease the number of cells, but also of the range of different cells. Both very large as well as very small cells are excluded.

In the neighborhood of $\delta = 0$ the spectrum is concentrated in a small interval around the crowding index α_p of the central cell. This means that every cell is surrounded by cells having almost the same size leading to some kind of clustering of cells of nearly equal size. So there appear in the neighborhood of very large cells no very small cells and vice versa. Of course, due to the symmetry of the probability distributions for the input patterns, these “clusters” of nearly equally sized cells are isotropically located in coupling space.

VII. SUMMARY

In the present paper we have analyzed the internal structure of cell clusters having a given output overlap with a certain central cell. The calculation of the internal multifractal spectrum of such clusters allowed us to discuss various storage and generalization problems of noisy output data within one single unified approach. The analysis included both the case of a lazy student which is satisfied whenever he achieves some maximal error rate, as well as the case of an absent-minded teacher offering incorrect data to his student. In the global cell spectrum of the whole coupling space it was not possible to give an interpretation to cells of crowding indices in-between the Gardner value α_0 and the generalization value α_1 . As a result of the present approach we are able to understand at least a proper subset of these cells as related to generalization tasks with output noise. Additionally we have shown that every cell is surrounded by cells having nearly the same size. The range of realized sizes is increasing with decreasing overlap of the output sequences labeling the cells.

We are aware of the fact that the multifractal approach is plagued by the existence of replica symmetry breaking, but due to the technical difficulties of a calculation which includes four different kinds of replicas we restricted our analysis to the replica symmetric ansatz. The inclusion of replica symmetry breaking effects would surely change some of the calculated quantities, but the qualitative picture would probably remain unchanged.

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